

Figure 1-A

T. reesei *egl6* nucleotide sequence (coding and non-coding)

CCACGGGTCGAGCAGTGTCTCTCCTCACTGCTTCATGAAGGTCTCTCGAGTCCTTGCCCTTGTCTCTGGGGCCGT
CATCCTTGCCCATGCTGCCCTTTTCATGGAAGAACGTCAAGCTCGCGGGCGGGCGGTTCGTCCCGGCATCATCTTCCA
TCCCAAGACAAAAGGCGTAGCATATGCACGAACAGATATTGGCGGGCTGTACCGCTCAACGCCGACGACTCATGGACCGC
CGTCACGGATGGGATTGCTGATAATGCCGGCTGGCAAACTGGGGCATCGACGCTGTTCGCTTGATCCGCAGGACGATCA
AAAGGTATGCGCAGTCGGCATGTATACGAACAGCTGGGATCCGAGTAAATGAGCCATCATTCGCTCGTCAGACCCGG
CGCAACGTGGTCCTTCACCAAATTGCCCTTCAAAGTCGGGGTAAATGCCAGGACCGGAGCCGGAGAGCGTCTGGCTGT
CGATCCGGCCAACTCCAACATCATCTACTTTGGTGCTCGCTCAGGAAACGGCTCTTGAAAGTCTACGGACGGCGCGTGAC
CTTTTCCAAGGTCTCGTCGTTCACGGCAACTGGGACGTACATCCAGACCCGAGTGATTCCAACGGCTACAACAGCGACAA
GCAAGGACTCATGTGGGTACGTTCACTCAACAGCAGCAGACCGGGGAGCCACGTCTCGTATCTTTGTTGGCACGGC
TGATAACATCACTGCTTCAGTCTATGTGAGCAGAAATGCCGGCTCCACGTGGAGTGTGTACCGGGCAGCCAGGGAATA
CTTTCCCTCAAGGCGAAACTGCAGCCAGCAGAGAAAGCCTTGTATCTGACCTATTCGATGGCACAGGGCCGTATGATGG
CACACTTGGCTCAGTGTGGAGTACGACATTGCAGGGGAACTTGAAAGACATCACCCCTGTCTCTGGATCAGATCTATA
CTTTGGCTTTGGCGGCTTGGCTCGAATTGCAAAAGCCAGGAACCTTGTGTGTGCTTTTGAACCTCTTGGTGGCCAGA
TGCTCAGCTGTTTCGGTCGACCCGACTCTGGGACAAACATGGAGCCCGATCTGGCGGTGGCGAGCTATCCGACTGAGACCTA
TTACTACAGCATCTCAACTCCCAAGCACCGTGGATCAAGAACAACTTTATCGATGTGACGAGCGAGTCAACGTCGGATGG
TCTCATCAAGCGCTCGGCTGGATGATTGAGTCTCTCGAGATTGACCCCAACCGACAGCAACCACTGGCTCTACGGCACCGG
AATGACAACTTTGGCGGCCACGATCTCAACCACTGGGACACCGCCCAATGTGTCAATCCAATCACTGGCAGACGACAA
CGAGGAATTCTCCGTCCAGGACCTGGCTCTGCACCCGGGAGCGAGCTATTGGCCGCGAGTCGGAGACGACAAACGGCTT
CACCTTTGCCAGCAGAAAACGACCTCGGACATCGCCCGAGACGGTCTGGGCAACGCCCAACATGGGCCACCTCGACGAGCGT
CGACTACGCCGGAACTCGGTCAAGAGCGTCTCGCGTCCGCAACACCGCCGCGACGCAACAGGTGGCCATCTCGTCCGA
CGGCGGCGGACGTGGAGCATCGACTACGCGGCGGACACGTCCATGAACGGCGGCAACGGTGGCTATTTCGGCCGACGGCGA
CACGATCCTCTGGTCGACCGCTCGTCCGGCGTGACGCTCGCAGTTCCAGGGCAGCTTTGGCTCCGTCTCGAGCCCTGCC
CGCGGGCGCGTCAATCGCTCGGACAAAGAACCAACAGCTCTTACGCCGCTCCGGATCGACCTTTTACGTCAGCAA
GGACACGGCAGCAGCTTCAACGCGGGGCGCAAGCTGGCAGCGCAGGACGATCCGGGATATCGCTGCTCACCCGACCCAC
CGCGGCACGTTGTATGTCTCGACCGGACGTCCGCATATTCCGCTCCACAGACTCGGGCAGCACCTTTGGCCAAAGTCTCCAC
CGCCCTGACCAACACCTACCAGATCGCCCTGGGTGTGGGCTCAGGCTCGAACTGGAACCTGTATGCCCTTCGGCACCGGCC

GTACGGGGCTCGCCTCTACGCCAGTGGAGACAGGGGGCCCTCCTGGACGGACATCCAGGGCTCCAGGGCTTCGGCTCCAT
CGACAGCACCAAGTCCCGGCAGCGGACGACCGCCGGCAAAGTCTACGTGGCACCAACGGCCGGGGCGTCTTTTACGC
TCAGGGAACCGTCGGCGGGCGCACGGGGGGACTTCCTCGTCGACCAAGCAGAGCAGCAGTACCTCTTTCGCCAGCTC
GAGCACCAAGCTGAGTCGAGCGTTGTATCCACGACCCGGCTTCGACGGTGACTTCGTCGAGGACCAAGCTCGCCGCCGG
TCCACGGGGTCAGGGTCGCCGTCATTATGCTCAGTCGCGAGGGAATTGGGTGGACGGGGCCGACGCACTGTGTGGCGCC
GTATGTCGCCAGAAGCAGAAATGATTATTACCACTGTGTGATGCTTGAACTGCCAAGCTCACGAGGAGAGCTACAT
ACCCCTAGGCTCGCAGTAAAGAGCTCAAGCATCCGAAAGACCTAGTAGAGATCCAGTCAGATAATTATCCATTTGT
TTGAAATTAATGATCTTCTATTGAAAAAATAAAAAA

Figure 2-A

Predicted *T. reesei* egl6 amino acid sequence

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MKVSRVLALV LGAVIPAHAA FSWKNVKLGG GGFVPGIIF HPKTKGVAYA RTDIGGLYRL NADDSWTAVT
10      20      30      40      50      60      70

DGIADNAGWH NWGIDAVALD PQDDQKVYAA VGMYTNSWDP SNGAIIRSSD RGATWSFTNL PFKVGGNMPG
80      90      100     110     120     130     140

RGAGERLAVD PANSNIIYFG ARSGNGLWKS TDGGVTFSKV SSFTAATGTIYI PDPSDSNGYN SDKQGLMWVT
150     160     170     180     190     200     210

FDSTSSTTGG ATSRIFVGTA DNITASVYVS TNAGSTWSAV PGQPGKYFFH KAKLQPAEKA LYLTYSDDGTG
220     230     240     250     260     270     280

PYDGTILGSVW RYDIAGGTWK DITPVSGSDL YFGFGGLGLD LQKPGTLVVA SLNSWWPDAQ LFRSTDSGTT
290     300     310     320     330     340     350

WSPIWAWASY PTETYYYSIS TPKAPWIKNN FIDVTSESPS DGLIKRLGWM IESLEIDPTD SNHWLYGTGM
360     370     380     390     400     410     420

TIFGGHDLTN WDTRHNVS IQ SLADGIEEFS VQDLASAPGG SELLAAVGDD NGFTFASRND LGTSPQTVWA
430     440     450     460     470     480     490

TPTWATSTSV DYAGNSVKSV VRVGNTAGTQ VAISSDGGAT WSIDYAADTS MNGGTVAYSA DGDITLWSTA
500     510     520     530     540     550     560

SSGVQRSQFQ GSFASVSSLP AGAVIASDKK TNSVFYAGSG STFFVSKDTG SSFTRGPKLG SAGTIRDIAA
570     580     590     600     610     620     630

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TCFAT 4563200T

Figure 2-B

Predicted *T. reesei* egl6 amino acid sequence

HPTTAGTLYV	STDVGIFRST	DSGTTFGQVS	TALTNTYQIA	LGVGSGSNWN	LYAFGTGPSG	ARLYASGDSG	
640	650	660	670	680	690	700	
ASWTDIQGSQ	GFGSIDSTKV	AGSGSTAGQV	YVGINGRGVF	YAQGTVGGGT	GGTSSSTKQS	SSSTSSASSS	
710	720	730	740	750	760	770	
TTLRSSVVST	TRASTVTSSR	TSSAAGPTGS	GVAGHYAQCQ	GIGWTGPTQC	VAPYVCQKQN	DYYYQCV	
780	790	800	810	820	830	837	